

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101090,049A
Source: FEW16
Date Processed by STIC: 1-4-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/10/090,049A

TIME: 12:26:00

Input Set : A:\NIH133.1CP1C2.TXT

Output Set: N:\CRF4\01042005\J090049A.raw

4 <110> APPLICANT: Luyten, Frank P.
 5 Moos, Malcolm J.R.
 6 Hoang, Bang
 7 Wang, Shouwen
 9 <120> TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
 10 GROWTH-INDUCING FRZB PROTEIN
 12 <130> FILE REFERENCE: NIH133.1CP1C2
 14 <140> CURRENT APPLICATION NUMBER: US 10/090049A
 15 <141> CURRENT FILING DATE: 2002-02-28
 17 <150> PRIOR APPLICATION NUMBER: US 09/289,268
 18 <151> PRIOR FILING DATE: 1999-04-09
 20 <150> PRIOR APPLICATION NUMBER: PCT US97/18362
 21 <151> PRIOR FILING DATE: 1997-10-08
 23 <150> PRIOR APPLICATION NUMBER: US 08/822333
 24 <151> PRIOR FILING DATE: 1997-03-20
 26 <150> PRIOR APPLICATION NUMBER: US 08/729,452
 27 <151> PRIOR FILING DATE: 1996-10-11
 29 <160> NUMBER OF SEQ ID NOS: 23
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 2374
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Bos taurus
 38 <400> SEQUENCE: 1
 39 aatagatgcc gcggcccgag aagtcttaga cgtcgggaaa gagcagccgg agaggcaggg 60
 40 gcggcgccgg ctggcgctcg gcgcagcttt tgggacccca ttgagggaa ttgatccaag 120
 41 gaagctgtga gattgccggg ggaggagaag ctcccatatc attgtgtcca cttccagggc 180
 42 ggggaggagg aaacggcgga gcgggcctct cggcgttctc cgcactgctg caccctgcc 240
 43 catcctgccg agatcatggt ctgcgggagc cgaggcgga tgetgctgct gccggccggg 300
 44 ctactcgccc tggtgcgct ctgcctgctc cgcgtgccc gagcgcgggc ggccgcctgt 360
 45 gagcccgctt gcattccct gtgcaagtcc ctgccctgga acatgactaa gatgccaac 420
 46 cacctgcacc acagcaccca ggccaacgcc atcctggcca tcgagcagtt cgaaggtctg 480
 47 ctgggcaccc actgcagccc ggatctgctc ttcttctct gtgctatgta cgcgcccac 540
 48 tgcaccattg acttccagca cgagcccatc aagccctgca agtctgtgtg cgagcgggcc 600
 49 cggcagggct gtgagcccat cctcatcaag taccgccact cgtggccgga aagcctggcc 660
 50 tgcgaggagc tgccagtata tgaccgcggc gtgtgcatct ctccggaggc catcgctact 720
 51 gccgacggag ccgattttcc tatggattcc agtaatggaa actgtagagg agcaagcagt 780
 52 gaacgctgca aatgtaaacc agtcagagct acacagaaga cctatttccg aaacaattac 840
 53 aactatgtca ttcgggctaa agttaagaa ataaagacca agtgtcatga tgtgactgca 900
 54 gtagtgagg tgaaggagat tttaaaggct tctctggtaa acattccaag ggaaactgtg 960
 55 aacctttata ccagctctgg ctgcctgtgt cctccactta acgttaatga ggagtatctc 1020
 56 atcatgggct acgaagatga agagcgctcc agattactgt tggtagaagg ttctattgct 1080
 57 gagaaatgga aggatcgact tggtaaaaaa gttaagcggg gggatatgaa gctccgtcat 1140

(ps.6)

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58 cttggactga atacaagtga ttctagccat agtgattcca ctcagagtca gaagcctggc 1200
59 aggaattcta actcccgga agcacgcaac taaatcctga aatgcagaaa atcctcagtg 1260
60 gacttcctat taagacttgc attgctggac tagcaaaggc aaattgcact attgcacgtc 1320
61 atagtctatt ttttagccac aaaaatcagg tggtaactga tattacttct attttttctt 1380
62 ttgttttctg cttttctcct tccccattc cttttttgt ggtctgagta cagatcctta 1440
63 aatatattat atgtattcta tttcactaat catgggaaaa ctgttctttg caataataat 1500
64 aaattaaaca tgttgatacc agggcctctt tgctggagta aatgttaatt tgctgttctg 1560
65 caccagatt gggaatgcaa tattggatgc aaagagagat ttctggtata cagagaaagc 1620
66 tagataggct gtaaagcata ctttgctgat ctaattacag cctcattctt gcatgccttt 1680
67 tggcattctc ctcacgctta gaaagttcta aatgtttata aaggtaaaat gacagtttga 1740
68 aatcaaagtc caacaggcag agcaatcaag caccaggaag catttatgaa gaaatgacac 1800
69 atgagatgaa ttatttgcaa gattggcagg aagcaaaata aatagcatta ggagctgggg 1860
70 atagagcatt ttgcctgact gagaagcaca actgaagcta gtactgttg ggggtgtaac 1920
71 agcagcattt ttcttttgac gatacatttg tttgtctgtg aatatattga tcagcattag 1980
72 agcagtggtt tgtgaccaga catcaggtgt tatcagcata gctctgttta atttgcttcc 2040
73 ttttagatga acgcattggt gtcttttttt tcttctttta aaataaatct cccttgctgc 2100
74 atttgaccag gaaaagaaag catatatgca tgtgcaccgg gctgttattt ttaagatatg 2160
75 tagctctata aaacgctata gtcaaaagat ggtaaaatgt gcaagattct ggggtgtgtg 2220
76 attaattgtg gtgtgtccgc atacactcac actcaagctg aagtgaacga caggcctgtg 2280
77 cactggcctg cactttatca tttggatttg tgctgtttaa tgctcagtaa aatatgctta 2340
78 ataaaaggaa aaaaaaaaaa aaaaaaaaaa aaaa 2374

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80 <210> SEQ ID NO: 2

81 <211> LENGTH: 325

82 <212> TYPE: PRT

83 <213> ORGANISM: Bos taurus

85 <400> SEQUENCE: 2

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87 1 5 10 15
88 Leu Ala Leu Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
89 20 25 30
90 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
91 35 40 45
92 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
93 50 55 60
94 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
95 65 70 75 80
96 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
97 85 90 95
98 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
99 100 105 110
100 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
101 115 120 125
102 Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
103 130 135 140
104 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
105 145 150 155 160
106 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
107 165 170 175
108 Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg

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109          180          185          190
110 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
111          195          200          205
112 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
113          210          215          220
114 Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn Leu Tyr Thr Ser
115 225          230          235          240
116 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Leu Ile
117          245          250          255
118 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
119          260          265          270
120 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
121          275          280          285
122 Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr Ser Asp Ser Ser
123          290          295          300
124 His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg Asn Ser Asn Ser
125 305          310          315          320
126 Arg Gln Ala Arg Asn
127          325
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 1484
132 <212> TYPE: DNA
133 <213> ORGANISM: Homo sapiens
135 <400> SEQUENCE: 3
136 cggggcctgg gcggsagggg cgggtggctgg agctcggtaa agctcgtggg accccattgg 60
137 gggaatttga tccaaggaag cggtgattgc cgggggagga gaagctccca gatccttgtg 120
138 tccacttgca gcgggggagg cggagacgcg gagcgggcct tttggcgctc actgcgcggc 180
139 tgcaccctgc cccatcctgc cgggatcatg gtctgcggca gcccgggagg gatgctgctg 240
140 ctgcgggccc ggctgcttgc cctggctgct ctctgcctgc tccgggtgcc cggggctcgg 300
141 gctgcagcct gtgagcccg cgcacatccc ctgtgcaagt ccctgccctg gaacatgact 360
142 aagatgccca accacctgca ccacagcact caggccaacg ccatcctggc catcgagcag 420
143 ttcgaaggtc tgctgggcac ccaactgcag cccgatctgc tcttcttctt ctgtgccatg 480
144 tacgcgcccc tctgcaccat tgacttccag cacgagccca tcaagccctg taagtctgtg 540
145 tgcgagcggg cccggcaggg ctgtgagccc atactcatca agtaccgcca ctctgggccc 600
146 gagaacctgg cctgcgagga gctgccagtg tacgacaggg gcgtgtgcat ctctcccag 660
147 gccatcgtta ctgcggacgg agctgatttt cctatggatt ctagtaacgg aaactgtaga 720
148 ggggcaagca gtgaacgctg taaatgtaag cctattagag ctacacagaa gacctatttc 780
149 cggaacaatt acaactatgt cattcgggct aaagttaaag agataaagac taagtgccat 840
150 gatgtgactg cagtagtgga ggtgaaggag attctaaagt cctctctggg aaacattcca 900
151 cgggacactg tcaacctcta taccagctct ggctgcctct gccctccact taatgttaat 960
152 gaggaatata tcatcatggg ctatgaagat gaggaacgtt ccagattact cttgggtgaa 1020
153 ggctctatag ctgagaagtg gaaggatcga ctcggtaaaa agttaagcg ctgggatatg 1080
154 aagcttcgtc atcttgga ctgtaaaagt gattctagca atagtgattc cactcagagt 1140
155 cagaagtctg gcaggaactc gaacccccgg caagcacgca actaaatccc gaaatacaaa 1200
156 aagtaacaca gtggacttcc tattaagact tacttgcat gctggactag caaaggaaaa 1260
157 ttgcactatt gcacatcata ttctattgtt tactataaaa atcatgtgat aactgattat 1320
158 tactttctgt tctcttttgg tttctgcttc tctcttctct caaccctttt gtaatggttt 1380
159 gggggcagac tcttaagtat attgtgagtt ttctatttca ctaatcatga gaaaaactgt 1440
160 tcttttgcaa taataataaa ttaaacatgc tgttaaaaaa aaaa 1484

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162 <210> SEQ ID NO: 4
163 <211> LENGTH: 325
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 4
168 Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
169 1 5 10 15
170 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
171 20 25 30
172 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
173 35 40 45
174 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
175 50 55 60
176 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
177 65 70 75 80
178 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
179 85 90 95
180 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
181 100 105 110
182 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
183 115 120 125
184 Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
185 130 135 140
186 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
187 145 150 155 160
188 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
189 165 170 175
190 Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
191 180 185 190
192 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
193 195 200 205
194 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
195 210 215 220
196 Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
197 225 230 235 240
198 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
199 245 250 255
200 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
201 260 265 270
202 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
203 275 280 285
204 Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
205 290 295 300
206 Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
207 305 310 315 320
208 Arg Gln Ala Arg Asn
209 325
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 111

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Input Set : A:\NIH133.1CP1C2.TXT

Output Set: N:\CRF4\01042005\J090049A.raw

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214 <212> TYPE: PRT
215 <213> ORGANISM: Rattus norvegicus
217 <400> SEQUENCE: 5
218 Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala Tyr Asn Gln
219 1 5 10 15
220 Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu Asp Ala Gly
221 20 25 30
222 Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln Cys Ser Ala
223 35 40 45
224 Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val Cys Thr Val
225 50 55 60
226 Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu Arg Ala Gln
227 65 70 75 80
228 Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln Trp Pro Asp Thr
229 85 90 95
230 Leu Lys Cys Glu Lys Phe Pro Val His Gly Arg Gly Glu Leu Cys
231 100 105 110
234 <210> SEQ ID NO: 6
235 <211> LENGTH: 111
236 <212> TYPE: PRT
237 <213> ORGANISM: Drosophila melanogaster
239 <400> SEQUENCE: 6
240 Cys Glu Pro Ile Thr Ile Ser Ile Cys Lys Asn Ile Pro Tyr Asn Met
241 1 5 10 15
242 Thr Ile Met Pro Asn Leu Ile Gly His Thr Lys Gln Glu Glu Ala Gly
243 20 25 30
244 Leu Glu Val His Gln Phe Ala Pro Leu Val Lys Ile Gly Cys Ser Asp
245 35 40 45
246 Asp Leu Gln Leu Phe Leu Cys Ser Leu Tyr Val Pro Val Cys Thr Ile
247 50 55 60
248 Leu Glu Arg Pro Ile Pro Pro Cys Arg Ser Leu Cys Glu Ser Ala Arg
249 65 70 75 80
250 Val Cys Glu Lys Leu Met Lys Thr Tyr Asn Phe Asn Trp Pro Glu Asn
251 85 90 95
252 Leu Glu Cys Ser Lys Phe Pro Val His Gly Gly Glu Asp Leu Cys
253 100 105 110
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 319
258 <212> TYPE: PRT
259 <213> ORGANISM: Xenopus laevis
261 <400> SEQUENCE: 7
262 Met Ser Pro Thr Arg Lys Leu Asp Ser Phe Leu Leu Leu Val Ile Pro
263 1 5 10 15
264 Gly Leu Val Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
265 20 25 30
266 Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
267 35 40 45
268 Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
269 50 55 60

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/04/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 21
Seq#:11; N Pos. 10,16
Seq#:12; Xaa Pos. 13

VERIFICATION SUMMARY

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L:378 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:382 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:393 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:408 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:412 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0